SEQUENCE LISTING

<110> JOHNS HOPKINS UNIVERSITY

<120> ENHANCEMENT OF ADENOVIRAL ONCOLYTIC ACTIVITY IN
      PROSTATE CELLS BY MODIFICATION OF THE E1A GENE PRODUCT

<130> 71699/59562-PCT

<140> PCT/US03/25171
<141> 2003-08-08

<150> 60/401,919
<151> 2002-08-08

<160> 22

<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence: Synthetic
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cttaagcagc tgctccgctg accttaaaga catcctgagc gaggccagca ccatgcaact 1320
ccttcagcaa cagcagcagg aagcagtatc cgaaggcagc agcagcggga gagcgaggga 1380
ggcctcgggg gctcccactt cctccaagga caattactta gggggcactt cgaccatttc 1440
tgacaacgcc aaggagttgt gtaaggcagt gtcggtgtcc atgggcctgg gtgtggaggc 1500
gttggagcat ctgagtccag gggaacagct tcgggggat tgcatgtacg ccccactttt 1560
gggagttcca cccgctgtgc gtcccactcc ttgtgcccca ttggccgaat gcaaaggttc 1620
tctgctagac gacagcgcag gcaagagcac tgaagatact gctgagtatt cccctttcaa 1680
gggaggttac accaaagggc tagaaggcga gagcctaggc tgctctggca gcgctgcagc 1740
agggagctcc gggacacttg aactgccgtc taccctgtct ctctacaagt ccggagcact 1800
ggacgaggca gctgcgtacc agagtcgcga ctactacaac tttccactgg ctctggccgg 1860
accgccgccc cctccgccgc ctccccatcc ccacgctcgc atcaagctgg agaacccgct 1920
ggactacggc agcgcctggg cggctgcggc ggcgcagtgc cgctatgggg acctggcgag 1980
cctgcatggc gcgggtgcag cgggacccgg ttctgggtca ccctcagccg ccgcttcctc 2040
atcctggcac actctcttca cagccgaaga aggccagttg tatggaccgt gtggtggtgg 2100
tggggggtggt ggcggcggcg gcggcggcgg cggcggcggc ggcggcggcg gcggcggcgg 2160
cggcgaggcg ggagctgtag ccccctacgg ctacactcgg cccctcagg ggctggcggg 2220
ccaggaaagc gacttcaccg cacctgatgt gtggtaccct ggcggcatgg tgagcagagt 2280
gccctatccc agtcccactt gtgtcaaaag cgaaatgggc ccctggatgg atagctactc 2340
cggaccttac ggggacatgc gtttggagac tgccagggac catgttttgc ccattgacta 2400
ttactttcca ccccagaaga cctgcctgat ctgtggagat gaagcttctg ggtgtcacta 2460
tggagctctc acatgtggaa gctgcaaggt cttcttcaaa agagccgctg aagggaaaca 2520
gaagtacctg tgcgccagca gaaatgattg cactattgat aaattccgaa ggaaaaattg 2580
tccatcttgt cgtcttcgga aatgttatga agcaggatg actctgggag cccggaagct 2640
gaagaaactt ggtaatctga aactacagga ggaaggagag gcttccagca ccaccagccc 2700
cactgagtga ctcgag 2716
```

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<210> 6
<211> 1051
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence construct 12S/DBD

<400> 6
accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccaacgag gaggcggttt cgcagatttt tcccgactct gtaatgttgg cggtgcagga 240
agggattgac ttactcactt ttccgccggc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggaggtg atcgatctta cctgccacga ggctggcttt ccacccagtg acgacgagga 420
tgaagagggt cctgtgtctg aacctgagcc tgagcccgag ccagaaccgg agcctgcaag 480
acctacccgc cgtcctaaaa tggcgcctgc tatcctgaga cgcccgacat cacctgtgtc 540
tagagaatgc aatagtagta cggatagctg tgactccggt ccttctaaca cacctcctga 600
gatacacccg gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg 660
tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac ctttggactt 720
gagctgtaaa cgccccaggc cagcggccgc aaagacctgc ctgatctgtg gagatgaagc 780
ttctgggtgt cactatggag ctctcacatg tggaagctgc aaggtcttct tcaaaagagc 840
cgctgaaggg aaacagaagt acctgtgcgc cagcagaaat gattgcacta ttgataaatt 900
ccgaaggaaa aattgtccat cttgtcgtct tcggaaatgt tatgaagcag ggatgactct 960
gggagcccgg aagctgaaga aacttggtaa tctgaaacta caggaggaag gagaggcttc 1020
cagcaccacc agccccactg agtgactcga g                                 1051


<210> 7
<211> 1164
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      amino acid sequence construct 12S/AR

<400> 7
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
 1               5                  10                  15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
            20                  25                  30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
            35                  40                  45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
        50                  55                  60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65                  70                  75                  80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
                85                  90                  95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
          100                105                  110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
          115                120              125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Pro Val Ser Glu Pro
          130                135              140

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg
145                  150              155              160

Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser
          165                170              175

Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn
          180                185              190

Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro
          195                200              205

Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu
        210              215              220

Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg
225                  230              235              240

Pro Arg Pro Ala Ala Ala Glu Val Gln Leu Gly Leu Gly Arg Val Tyr
          245              250              255

Pro Arg Pro Pro Ser Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe
          260              265              270

Gln Ser Val Arg Glu Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu
          275              280              285

Ala Ala Ser Ala Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln
        290            295              300

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
305                  310              315              320

Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu
          325              330              335

Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val
          340              345              350

Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys
        355            360              365

His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala
        370            375              380

Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp
385           390           395           400

Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly
          405           410           415

Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser
          420           425           430

Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly
          435           440           445

Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser
    450           455           460

Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys
465           470           475           480

Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala
          485           490           495

Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr
          500           505           510

Ala Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala
          515           520           525

Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys
    530           535           540

Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr
545           550           555           560

Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala
          565           570           575

Gly Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys
          580           585           590

Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr
    595           600           605

Asn Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro
    610           615           620

His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser
625           630           635           640

Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser
          645           650           655

Leu His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala
          660           665           670

Ala Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln
      675            680            685

Leu Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
    690            695            700

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly
705            710          715          720

Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly
          725          730          735

Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met
          740          745          750

Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met
    755          760          765

Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu
    770          775          780

Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro
785            790          795          800

Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr
          805          810          815

Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala
          820          825          830

Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile
          835          840          845

Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys
    850          855          860

Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly
865            870          875          880

Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro
          885          890          895

Thr Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr
          900          905          910

Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly
          915          920          925

Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala
    930          935          940

Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val
945            950          955          960

Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp
                965            970               975

Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe
                980             985             990

Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr
            995         1000            1005

Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg
     1010            1015            1020

Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly
1025            1030            1035            1040

Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu
            1045            1050            1055

Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe
            1060            1065            1070

Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala
     1075            1080            1085

Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu
     1090            1095            1100

Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln
1105            1110            1115            1120

Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe
            1125            1130            1135

Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu
            1140            1145            1150

Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln
     1155            1160

<210> 8
<211> 898
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      amino acid sequence construct 12S/TAD

<400> 8
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1               5               10              15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
           20                  25                  30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
           35                 40                  45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
     50                  55                  60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gln Ile Asp Leu
65                  70               75              80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
               85               90              95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
          100               105            110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
        115              120           125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Pro Val Ser Glu Pro
     130              135              140

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg
145              150           155            160

Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser
          165             170           175

Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn
          180             185          190

Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro
        195              200          205

Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu
     210              215            220

Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg
225             230           235           240

Pro Arg Pro Ala Ala Ala Glu Val Gln Leu Gly Leu Gly Arg Val Tyr
             245            250          255

Pro Arg Pro Pro Ser Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe
          260             265          270

Gln Ser Val Arg Glu Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu
        275              280          285

Ala Ala Ser Ala Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln
     290              295            300

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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
305             310             315             320

Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu
                325             330             335

Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val
            340             345             350

Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys
        355             360             365

His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala
    370             375             380

Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp
385             390             395             400

Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly
            405             410             415

Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser
            420             425             430

Thr Met Gln Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly
        435             440             445

Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser
    450             455             460

Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys
465             470             475             480

Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala
            485             490             495

Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr
        500             505             510

Ala Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala
        515             520             525

Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys
        530             535             540

Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr
545             550             555             560

Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala
            565             570             575

Gly Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys
            580             585             590
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Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr
    595                600                605

Asn Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro
    610                615                620

His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser
625                630            635              640

Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser
           645             650              655

Leu His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala
           660            665            670

Ala Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln
         675           680           685

Leu Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
    690           695           700

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly
705                710            715              720

Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly
           725           730              735

Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met
         740           745           750

Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met
       755           760           765

Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu
    770           775           780

Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro
785              790            795            800

Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr
         805           810           815

Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala
         820           825           830

Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile
       835           840           845

Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys
    850           855           860

Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly
865              870            875            880

Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro
                885               890               895

Thr Glu


<210> 9
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      amino acid sequence construct 12S/DBD

<400> 9
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
  1               5                  10                  15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
          20                  25                  30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
          35                  40                  45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
    50                  55                  60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65                  70                  75                  80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
              85                  90                  95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
          100                 105                 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
          115                 120                 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Pro Val Ser Glu Pro
    130                 135                 140

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg
145                 150                 155                 160

Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser
              165                 170                 175

Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn
              180                 185                 190

Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro
    195             200         205

Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu
    210             215         220

Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg
225             230         235             240

Pro Arg Pro Ala Ala Ala Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala
            245         250             255

Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe
        260         265         270

Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg
    275             280         285

Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys
    290             295         300

Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys
305             310         315             320

Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser
            325             330             335

Ser Thr Thr Ser Pro Thr Glu
            340


<210> 10
<211> 986
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence construct EA1

<400> 10
atgagacata ttatctgcca cggaggtgtt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctcctagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agattttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
ctcactttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag 300
cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgacg acgaggatga gagggtgag 420
gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480
cggaggaata cggggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600
tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt 780

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ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccc ggtggtcccg ctgtgcccca ttaaaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataa                                      986
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<210> 11
<211> 986
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence construct EA1/TAD

<400> 11
atgagacata ttatctgcca cggaggtgtt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctcctagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agattttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
ctcactttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag 300
cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgacg acgaggatga gagggtgag 420
gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480
cggaggaata cggggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600
tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaatttttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccc ggtggtcccg ctgtgcccca ttaaaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataa                                      986
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<210> 12
<211> 1022
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence construct EA1/AR

<400> 12
atgagacata ttatctgcca cggaggtgtt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctcctagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agattttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
ctcactttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag 300
cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgacg acgaggatga gagggtgag 420
gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480
cggaggaata cggggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
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atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600
tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccc ggtggtcccg ctgtgcccca ttaaaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataagcgg ccgcagaagt gcagttaggg ctgggaaggg 1020
tc                                                                 1022
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<210> 13
<211> 1022
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        nucleotide sequence construct EA1/AR(C685Y)

<400> 13
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cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agattttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
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cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggcttttcca cccagtgacg acgaggatga agagggtgag 420
gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600
tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660
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gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
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gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataagcgg ccgcagaagt gcagttaggg ctgggaaggg 1020
tc                                                                 1022
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<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        primer

<400> 14
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<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 15
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<210> 16
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 16
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<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 17
tcactcctcg agtcactggg tgtggaaata gatgggctt                       39


<210> 18
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 18
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<213> Artificial Sequence

<220>
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<400> 19
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<212> DNA
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<220>
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<400> 20
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<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 21
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<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
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      primer

<400> 22
cgggatccga ggtcagatgt aaccaaga                               28
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